

SEQUENCE LISTING

<110> Kinch, Michael S.

<120> EphA2 VACCINES

<130> 10271-148

<150> US 60/532,696

<151> 2003-12-24

<150> US 60/602,588

<151> 2004-08-18

<150>

<151> 2004-10-01

<150>

<151> 2004-10-07

<160> 72

<170> PatentIn version 3.2

<210> 1

<211> 3963

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138)..(3068)

<400> 1

attaaggact cggggcagga ggggcagaag ttgcgcgcag gccggcgggc gggagcggac 60

accgaggccg gcgtgcaggc gtgcgggtgt gcgggagccg ggctcggggg gatcggaccg 120

agagcgagaa gcgcggc atg gag ctc cag gca gcc cgc gcc tgc ttc gcc 170

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala
1 5 10

ctg ctg tgg ggc tgt gcg ctg gcc gcg gcc gcg gcg gcg cag ggc aag 218

Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys
15 20 25

gaa gtg gta ctg ctg gac ttt gct gca gct gga ggg gag ctc ggc tgg 266

Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp
30 35 40

ctc aca cac ccg tat ggc aaa ggg tgg gac ctg atg cag aac atc atg 314

Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met
45 50 55

aat gac atg ccg atc tac atg tac tcc gtg tgc aac gtg atg tct ggc 362

Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
60 65 70 75

gac cag gac aac tgg ctc cgc acc aac tgg gtg tac cga gga gag gct 410

Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala

80					85					90						
gag	cgt	atc	ttc	att	gag	ctc	aag	ttt	act	gta	cgt	gac	tgc	aac	agc	458
Glu	Arg	Ile	Phe	Ile	Glu	Leu	Lys	Phe	Thr	Val	Arg	Asp	Cys	Asn	Ser	
95					100					105						
ttc	cct	ggg	ggc	gcc	agc	tcc	tgc	aag	gag	act	ttc	aac	ctc	tac	tat	506
Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	
110					115					120						
gcc	gag	tcg	gac	ctg	gac	tac	ggc	acc	aac	ttc	cag	aag	cgc	ctg	ttc	554
Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	Thr	Asn	Phe	Gln	Lys	Arg	Leu	Phe	
125					130					135						
acc	aag	att	gac	acc	att	gcg	ccc	gat	gag	atc	acc	gtc	agc	agc	gac	602
Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	Asp	Glu	Ile	Thr	Val	Ser	Ser	Asp	
140					145					150						
ttc	gag	gca	cgc	cac	gtg	aag	ctg	aac	gtg	gag	gag	cgc	tcc	gtg	ggg	650
Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	Glu	Glu	Arg	Ser	Val	Gly	
160					165					170						
ccg	ctc	acc	cgc	aaa	ggc	ttc	tac	ctg	gcc	ttc	cag	gat	atc	ggg	gcc	698
Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	
175					180					185						
tgt	gtg	gcg	ctg	ctc	tcc	gtc	cgt	gtc	tac	tac	aag	aag	tgc	ccc	gag	746
Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	
190					195					200						
ctg	ctg	cag	ggc	ctg	gcc	cac	ttc	cct	gag	acc	atc	gcc	ggc	tct	gat	794
Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	
205					210					215						
gca	cct	tcc	ctg	gcc	act	gtg	gcc	ggc	acc	tgt	gtg	gac	cat	gcc	gtg	842
Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val	
220					225					230						
gtg	cca	ccg	ggg	ggg	gaa	gag	ccc	cgt	atg	cac	tgt	gca	gtg	gat	ggc	890
Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly	
240					245					250						
gag	tgg	ctg	gtg	ccc	att	ggg	cag	tgc	ctg	tgc	cag	gca	ggc	tac	gag	938
Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	
255					260					265						
aag	gtg	gag	gat	gcc	tgc	cag	gcc	tgc	tgc	cct	gga	ttt	ttt	aag	ttt	986
Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	
270					275					280						
gag	gca	tct	gag	agc	ccc	tgc	ttg	gag	tgc	cct	gag	cac	acg	ctg	cca	1034
Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	
285					290					295						
tcc	cct	gag	ggg	gcc	acc	tcc	tgc	gag	tgt	gag	gaa	ggc	ttc	ttc	cgg	1082
Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	
300					305					310						
gca	cct	cag	gac	cca	gcg											

cca	cac	tac	ctc	aca	gcc	gtg	ggc	atg	ggt	gcc	aag	gtg	gag	ctg	cgc	1178
Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	
			335					340					345			
tgg	acg	ccc	cct	cag	gac	agc	ggg	ggc	cgc	gag	gac	att	gtc	tac	agc	1226
Trp	Thr	Pro	Pro	Gln	Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	
		350					355					360				
gtc	acc	tgc	gaa	cag	tgc	tgg	ccc	gag	tct	ggg	gaa	tgc	ggg	ccg	tgt	1274
Val	Thr	Cys	Glu	Gln	Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	
	365					370					375					
gag	gcc	agt	gtg	cgc	tac	tcg	gag	cct	cct	cac	gga	ctg	acc	cgc	acc	1322
Glu	Ala	Ser	Val	Arg	Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	
380				385						390					395	
agt	gtg	aca	gtg	agc	gac	ctg	gag	ccc	cac	atg	aac	tac	acc	ttc	acc	1370
Ser	Val	Thr	Val	Ser	Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	
			400						405					410		
gtg	gag	gcc	cgc	aat	ggc	gtc	tca	ggc	ctg	gta	acc	agc	cgc	agc	ttc	1418
Val	Glu	Ala	Arg	Asn	Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe	
		415						420				425				
cgt	act	gcc	agt	gtc	agc	atc	aac	cag	aca	gag	ccc	ccc	aag	gtg	agg	1466
Arg	Thr	Ala	Ser	Val	Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg	
		430					435					440				
ctg	gag	ggc	cgc	agc	acc	acc	tcg	ctt	agc	gtc	tcc	tgg	agc	atc	ccc	1514
Leu	Glu	Gly	Arg	Ser	Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	
	445					450					455					
ccg	ccg	cag	cag	agc	cga	gtg	tgg	aag	tac	gag	gtc	act	tac	cgc	aag	1562
Pro	Pro	Gln	Gln	Ser	Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	
460				465						470					475	
aag	gga	gac	tcc	aac	agc	tac	aat	gtg	cgc	cgc	acc	gag	ggt	ttc	tcc	1610
Lys	Gly	Asp	Ser	Asn	Ser	Tyr	Asn	Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	
			480						485					490		
gtg	acc	ctg	gac	gac	ctg	gcc	cca	gac	acc	acc	tac	ctg	gtc	cag	gtg	1658
Val	Thr	Leu	Asp	Asp	Leu	Ala	Pro	Asp	Thr	Thr	Tyr	Leu	Val	Gln	Val	
		495						500					505			
cag	gca	ctg	acg	cag	gag	ggc	cag	ggg	gcc	ggc	agc	aag	gtg	cac	gaa	1706
Gln	Ala	Leu	Thr	Gln	Glu	Gly	Gln	Gly	Ala	Gly	Ser	Lys	Val	His	Glu	
		510					515					520				
ttc	cag	acg	ctg	tcc	ccg	gag	gga	tct	ggc	aac	ttg	gcg	gtg	att	ggc	1754
Phe	Gln	Thr	Leu	Ser	Pro	Glu	Gly	Ser	Gly	Asn	Leu	Ala	Val	Ile	Gly	
	525					530					535					
ggc	gtg	gct	gtc	ggt	gtg	gtc	ctg	ctt	ctg	gtg	ctg	gca	gga	gtt	ggc	1802
Gly	Val	Ala	Val	Gly	Val	Val	Leu	Leu	Leu	Val	Leu	Ala	Gly	Val	Gly	
540				545						550					555	
ttc	ttt	atc	cac	cgc	agg	agg	aag	aac	cag	cgt	gcc	cgc	cag	tcc	ccg	1850
Phe	Phe	Ile	His	Arg	Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	
			560						565					570		

gag gac gtt tac ttc tcc aag tca gaa caa ctg aag ccc ctg aag aca	1898
Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr	
575 580 585	
tac gtg gac ccc cac aca tat gag gac ccc aac cag gct gtg ttg aag	1946
Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys	
590 595 600	
ttc act acc gag atc cat cca tcc tgt gtc act cgg cag aag gtg atc	1994
Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys Val Ile	
605 610 615	
gga gca gga gag ttt ggg gag gtg tac aag ggc atg ctg aag aca tcc	2042
Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser	
620 625 630 635	
tcg ggg aag aag gag gtg ccg gtg gcc atc aag acg ctg aaa gcc ggc	2090
Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly	
640 645 650	
tac aca gag aag cag cga gtg gac ttc ctc ggc gag gcc ggc atc atg	2138
Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met	
655 660 665	
ggc cag ttc agc cac cac aac atc atc cgc cta gag ggc gtc atc tcc	2186
Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser	
670 675 680	
aaa tac aag ccc atg atg atc atc act gag tac atg gag aat ggg gcc	2234
Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala	
685 690 695	
ctg gac aag ttc ctt cgg gag aag gat ggc gag ttc agc gtg ctg cag	2282
Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln	
700 705 710 715	
ctg gtg ggc atg ctg cgg ggc atc gca gct ggc atg aag tac ctg gcc	2330
Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala	
720 725 730	
aac atg aac tat gtg cac cgt gac ctg gct gcc cgc aac atc ctc gtc	2378
Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val	
735 740 745	
aac agc aac ctg gtc tgc aag gtg tct gac ttt ggc ctg tcc cgc gtg	2426
Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val	
750 755 760	
ctg gag gac gac ccc gag gcc acc tac acc acc agt ggc ggc aag atc	2474
Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile	
765 770 775	
ccc atc cgc tgg acc gcc ccg gag gcc att tcc tac cgg aag ttc acc	2522
Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr	
780 785 790 795	
tct gcc agc gac gtg tgg agc ttt ggc att gtc atg tgg gag gtg atg	2570
Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu Val Met	
800 805 810	
acc tat ggc gag cgg ccc tac tgg gag ttg tcc aac cac gag gtg atg	2618

Thr	Tyr	Gly	Glu	Arg	Pro	Tyr	Trp	Glu	Leu	Ser	Asn	His	Glu	Val	Met	
			815					820					825			
aaa gcc atc aat gat ggc ttc cgg ctc ccc aca ccc atg gac tgc ccc	2666															
Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro																
	830						835					840				
tcc gcc atc tac cag ctc atg atg cag tgc tgg cag cag gag cgt gcc	2714															
Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala																
	845					850					855					
cgc cgc ccc aag ttc gct gac atc gtc agc atc ctg gac aag ctc att	2762															
Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile																
860					865				870					875		
cgt gcc cct gac tcc ctc aag acc ctg gct gac ttt gac ccc cgc gtg	2810															
Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val																
			880					885						890		
tct atc cgg ctc ccc agc acg agc ggc tgc gag ggg gtg ccc ttc cgc	2858															
Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg																
	895						900						905			
acg gtg tcc gag tgg ctg gag tcc atc aag atg cag cag tat acg gag	2906															
Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu																
	910					915						920				
cac ttc atg gcg gcc ggc tac act gcc atc gag aag gtg gtg cag atg	2954															
His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met																
	925					930					935					
acc aac gac gac atc aag agg att ggg gtg cgg ctg ccc ggc cac cag	3002															
Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln																
940					945				950					955		
aag cgc atc gcc tac agc ctg ctg gga ctc aag gac cag gtg aac act	3050															
Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr																
	960						965						970			
gtg ggg atc ccc atc tga gcctcgacag ggctggagc cccatcggcc	3098															
Val Gly Ile Pro Ile																
	975															
aagaatactt gaagaaacag agtggcctcc ctgctgtgcc atgctgggcc actggggact	3158															
ttattttattt ctagttcttt cctccccctg caacttcgcg tgaggggtct cggatgacac	3218															
cctggcctga actgaggaga tgaccaggga tgctgggctg ggccctcttt ccctgcgaga	3278															
cgcacacagc tgagcactta gcaggcaccg ccacgtccca gcatccctgg agcaggagcc	3338															
ccgccacagc cttcggacag acatatagga tattcccaag ccgaccttcc ctccgccttc	3398															
tcccacatga ggccatctca ggagatggag ggcttggccc agcgccaagt aaacagggta	3458															
cctcaagccc catttcctca cactaagagg gcagactgtg aacttgactg ggtgagaccc	3518															
aaagcgggtcc ctgtccctct agtgccttct ttagaccctc gggccccatc ctcatccctg	3578															
actggccaaa cccttgcttt cctgggcctt tgcaagatgc ttggttgtgt tgaggttttt	3638															

```

aaatatatat tttgtacttt gtggagagaa tgtgtgtgtg tggcaggggg ccccgccagg 3698
gctgggggaca gaggggtgtca aacattcgtg agctgggggac tcagggaccg gtgctgcagg 3758
agtgtcctgc ccatgccccca gtcggccccca tctctcatcc ttttggataa gtttctattc 3818
tgtcagtgtt aaagattttg ttttgttggga cttttttttc gaatcttaat ttattatttt 3878
tttttatattt attgttagaa aatgacttat ttctgctctg gaataaagtt gcagatgatt 3938
caaaccgaaa aaaaaaaaaa aaaaaa 3963

```

```

<210> 2
<211> 976
<212> PRT
<213> Homo sapiens
<400> 2

```

```

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys
1 5 10 15

```

```

Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu
20 25 30

```

```

Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
35 40 45

```

```

Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
50 55 60

```

```

Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
65 70 75 80

```

```

Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile
85 90 95

```

```

Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala
100 105 110

```

```

Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
115 120 125

```

```

Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr
130 135 140

```

```

Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His
145 150 155 160

```

```

Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys

```

165										170					175				
Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu				
			180					185					190						
Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu				
		195					200					205							
Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala				
	210					215					220								
Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly				
225					230					235					240				
Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro				
				245					250					255					
Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala				
		260						265					270						
Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser				
		275					280					285							
Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala				
	290					295					300								
Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro				
305					310					315					320				
Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr				
				325					330					335					
Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln				
			340					345					350						
Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln				
		355					360					365							
Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg				
	370					375					380								
Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser				
385					390					395					400				
Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn				
				405					410					415					

Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val
 420 425 430

Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser
 435 440 445

Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser
 450 455 460

Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn
 465 470 475 480

Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp
 485 490 495

Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln
 500 505 510

Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser
 515 520 525

Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly
 530 535 540

Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg
 545 550 555 560

Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
 565 570 575

Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
 580 585 590

Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
 595 600 605

His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
 610 615 620

Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
 625 630 635 640

Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
 645 650 655

Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
 660 665 670

His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
 675 680 685

Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu
 690 695 700

Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
 705 710 715 720

Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
 725 730 735

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
 740 745 750

Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
 755 760 765

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
 770 775 780

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
 785 790 795 800

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
 805 810 815

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
 820 825 830

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
 835 840 845

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
 850 855 860

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
 865 870 875 880

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
 885 890 895

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
 900 905 910

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
 915 920 925

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
 930 935 940

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
 945 950 955 960

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 965 970 975

<210> 3
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 3

Thr Leu Ala Asp Phe Asp Pro Arg Val Pro Arg Thr
 1 5 10

<210> 4
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 4

Val Leu Leu Leu Val Leu Ala Gly Val
 1 5

<210> 5
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 5

Val Leu Ala Gly Val Gly Phe Phe Ile
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 6

Ile Met Asn Asp Met Pro Ile Tyr Met
1 5

<210> 7
<211> 9
<212> PRT
<213> Homo sapiens

<400> 7

Ser Leu Leu Gly Leu Lys Asp Gln Val
1 5

<210> 8
<211> 9
<212> PRT
<213> Homo sapiens

<400> 8

Trp Leu Val Pro Ile Gly Gln Cys Leu
1 5

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<400> 9

Leu Leu Trp Gly Cys Ala Leu Ala Ala
1 5

<210> 10
<211> 9
<212> PRT
<213> Homo sapiens

<400> 10

Gly Leu Thr Arg Thr Ser Val Thr Val
1 5

<210> 11
<211> 9
<212> PRT
<213> Homo sapiens

<400> 11

Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
1 5

<210> 12

<211> 9
<212> PRT
<213> Homo sapiens

<400> 12

Lys Leu Asn Val Glu Glu Arg Ser Val
1 5

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

<400> 13

Ile Met Gly Gln Phe Ser His His Asn
1 5

<210> 14
<211> 9
<212> PRT
<213> Homo sapiens

<400> 14

Tyr Ser Val Cys Asn Val Met Ser Gly
1 5

<210> 15
<211> 9
<212> PRT
<213> Homo sapiens

<400> 15

Met Gln Asn Ile Met Asn Asp Met Pro
1 5

<210> 16
<211> 15
<212> PRT
<213> Homo sapiens

<400> 16

Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg
1 5 10 15

<210> 17
<211> 13
<212> PRT
<213> Homo sapiens

<400> 17

Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
 1 5 10

<210> 18
 <211> 16
 <212> PRT
 <213> Homo sapiens

<400> 18

Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser
 1 5 10 15

<210> 19
 <211> 3105
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct

<400> 19
 atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60
 caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
 ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggtatctc 180
 gagctccagg cagcccgcgc ctgcttcgcc ctgctgtggg gctgtgcgct ggccgcggcc 240
 gcggcgggcg agggcaagga agtggactg ctggactttg ctgcagctgg aggggagctc 300
 ggctggctca cacaccgta tggcaaaggg tgggacctga tgcagaacat catgaatgac 360
 atgccgatct acatgtactc cgtgtgcaac gtgatgtctg gcgaccagga caactggctc 420
 cgcaccaact ggggtgtacc aggagaggct gagcgtatct tcattgagct caagtttact 480
 gtacgtgact gcaacagctt ccttgggtgg gccagctcct gcaaggagac tttcaacctc 540
 tactatgccg agtcggacct ggactacggc accaacttcc agaagcgcct gttcaccaag 600
 attgacacca ttgcgcccga tgagatcacc gtcagcagcg acttcgaggc acgccacgtg 660
 aagctgaacg tggaggagcg ctccgtgggg ccgctcaccc gcaaaggctt ctacctggcc 720
 ttccaggata tcggtgcctg tgtggcgctg ctctccgtcc gtgtctacta caagaagtgc 780
 cccgagctgc tgcagggcct ggcccacttc cctgagacca tcgccggctc tgatgcacct 840
 tccctggcca ctgtggccgg cacctgtgtg gaccatgccg tgggtgccacc ggggggtgaa 900
 gagccccgta tgcactgtgc agtggatggc gagtggctgg tgcccattgg gcagtgcctg 960
 tgccaggcag gctacgagaa ggtggaggat gcctgccagg cctgctcgcc tggatttttt 1020
 aagtttgagg catctgagag cccctgcttg gagtgccttg agcacacgct gccatccctt 1080

gaggggtgcca cctcctgcga gtgtgaggaa ggcttcttcc gggcacctca ggacccagcg	1140
tcgatgcctt gcacacgacc cccctcggcc ccacactacc tcacagccgt gggcatgggt	1200
gccaaggtgg agctgcgctg gacgccccct caggacagcg ggggccgca ggacattgtc	1260
tacagcgta cctgcgaaca gtgctggccc gagtctgggg aatgcggggc gtgtgaggcc	1320
agtgtgcgct actcggagcc tctcacgga ctgaccgca ccagtgtgac agtgagcgac	1380
ctggagcccc acatgaacta caccttcacc gtggaggccc gcaatggcgt ctcaggcctg	1440
gtaaccagcc gcagcttccg tactgccagt gtcagcatca accagacaga gcccccaag	1500
gtgaggctgg agggccgcag caccacctcg cttagcgtct cctggagcat cccccgcg	1560
cagcagagcc gagtgtggaa gtacgaggtc acttaccgca agaagggaga ctccaacagc	1620
tacaatgtgc gccgcaccga gggtttctcc gtgaccctgg acgacctggc ccagacacc	1680
acctacctgg tccaggtgca ggcactgacg caggaggggc agggggccgg cagcagggtg	1740
cacgaattcc agacgtgtc cccggaggga tctggcaact tggcggatgat tggcggcgtg	1800
gctgtcgggtg tggctctgct tctggtgctg gcaggagtgt gcttctttat ccaccgcagg	1860
aggaagaacc agcgtgcccg ccagtcctcg gaggacgttt acttctccaa gtcagaacaa	1920
ctgaagcccc tgaagacata cgtggacccc cacacatatg aggaccccaa ccaggctgtg	1980
ttgaagttca ctaccgagat ccatccatcc tgtgtcactc ggcagaaggt gatcggagca	2040
ggagagtttg gggaggtgta caagggcagc ctgaagacat cctcggggaa gaaggaggtg	2100
ccggtggcca tcaagacgct gaaagccggc tacacagaga agcagcgagt ggaacttctc	2160
ggcgaggccg gcatcatggg ccagttcagc caccacaaca tcatccgcct agagggcgtc	2220
atctccaaat acaagcccat gatgatcatc actgagtaca tggagaatgg ggcctggac	2280
aagttccttc gggagaagga tggcgagttc agcgtgctgc agctggtggg catgctgcgg	2340
ggcatcgag ctggcatgaa gtacctggcc aacatgaact atgtgcaccg tgacctggct	2400
gcccgaaca tctctgtcaa cagcaacctg gtctgcaagg tgtctgactt tggcctgtcc	2460
cgctgctggg aggcagaccc cgaggccacc tacaccacca gtggcggaac gatccccatc	2520
cgctggaccg ccccgaggc catttctac cggaagttca cctctgccag cgacgtgtgg	2580
agctttggca ttgtcatgtg ggaggtgatg acctatggcg agcgcccta ctgggagttg	2640
tccaaccacg aggtgatgaa agccatcaat gatggcttcc ggctccccac acctatggac	2700
tgccccctcg ccatctacca gctcatgatg cagtgtgtgg agcaggagcg tgccccccgc	2760
cccaagttcg ctgacatcgt cagcatcctg gacaagctca ttcgtgcccc tgactccctc	2820
aagaccctgg ctgactttga cccccgctg tctatccggc tccccagcac gagcggctcg	2880
gaggggggtgc ccttcgcgac ggtgtccgag tggctggagt ccatcaagat gcagcagtat	2940

acggagcact tcattggcggc cggctacact gccatcgaga aggtggtgca gatgaccaac 3000
gacgacatca agaggattgg ggtgcggtg cccggccacc agaagcgcat cgcctacagc 3060
ctgctgggac tcaaggacca ggtgaacact gtggggatcc ccatc 3105

<210> 20

<211> 1035

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 20

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Leu Gln Ala
50 55 60

Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala
65 70 75 80

Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala
85 90 95

Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp
100 105 110

Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val
115 120 125

Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp
130 135 140

Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr
145 150 155 160

Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu
165 170 175

Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn
 180 185 190

Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu
 195 200 205

Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu Asn Val
 210 215 220

Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala
 225 230 235 240

Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr
 245 250 255

Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu
 260 265 270

Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr
 275 280 285

Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met
 290 295 300

His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu
 305 310 315 320

Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser
 325 330 335

Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys
 340 345 350

Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys
 355 360 365

Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys
 370 375 380

Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly
 385 390 395 400

Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg
 405 410 415

Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser
 420 425 430

Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro
 435 440 445

His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His
 450 455 460

Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu
 465 470 475 480

Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr
 485 490 495

Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser
 500 505 510

Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr
 515 520 525

Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg
 530 535 540

Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr
 545 550 555 560

Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala
 565 570 575

Gly Ser Arg Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly
 580 585 590

Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu
 595 600 605

Val Leu Ala Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln
 610 615 620

Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln
 625 630 635 640

Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro
 645 650 655

Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val
 660 665 670

Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys
 675 680 685

Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile
 690 695 700

Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu
 705 710 715 720

Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg
 725 730 735

Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu
 740 745 750

Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly
 755 760 765

Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala
 770 775 780

Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala
 785 790 795 800

Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp
 805 810 815

Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr
 820 825 830

Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile
 835 840 845

Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile
 850 855 860

Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu
 865 870 875 880

Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro
 885 890 895

Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys

900 905 910
 Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser
 915 920 925
 Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala
 930 935 940
 Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser
 945 950 955 960
 Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys
 965 970 975
 Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile
 980 985 990
 Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val
 995 1000 1005
 Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly
 1010 1015 1020
 Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 1025 1030 1035

<210> 21
 <211> 1506
 <212> DNA
 <213> Homo sapiens

<400> 21
 cagggcaagg aagtgggtact gctggacttt gctgcagctg gaggggagct cggctggctc 60
 acacaccctgt atggcaaagg gtgggacctg atgcagaaca tcatgaatga catgccgatc 120
 tacatgtact ccgtgtgcaa cgtgatgtct ggcgaccagg acaactggct ccgcaccaac 180
 tgggtgtacc gaggagagggc tgagcgtatc ttcattgagc tcaagtttac tgtacgtgac 240
 tgcaacagct tccctgggtgg cgccagctcc tgcaaggaga ctttcaacct ctactatgcc 300
 gagtcggacc tggactacgg caccaacttc cagaagcgcc tgttcaccaa gattgacacc 360
 attgcgcccgt atgagatcac cgctcagcagc gacttcgagg cacgccacgt gaagctgaac 420
 gtggaggagc gctccgtggg gccgctcacc cgcaaaggct tctacctggc cttccaggat 480
 atcgggtgcct gtgtggcgct gctctccgtc cgtgtctact acaagaagtg ccccgagctg 540
 ctgcaggggcc tggcccactt ccctgagacc atcgccggct ctgatgcacc ttccctggcc 600

```

actgtggccg gcacctgtgt ggaccatgcc gtggtgccac cgggggggtga agagccccgt    660
atgcactgtg cagtggatgg cgagtggctg gtgccattg ggcagtgcct gtgccaggca    720
ggctacgaga aggtggagga tgcctgccag gcctgctcgc ctggattttt taagtttgag    780
gcatctgaga gcccctgctt ggagtgcctt gagcacacgc tgccatcccc tgagggtgcc    840
acctctgcg agtgtgagga aggtttcttc cgggcacctc aggaccagc gtcgatgcct    900
tgcacacgac cccctccgc cccacactac ctcacagccg tgggcatggg tgccaagggtg    960
gagctgcgct ggacgcccc tcaggacagc gggggccgcg aggacattgt ctacagcgtc   1020
acctgcgaac agtgctggcc cgagtctggg gaatgcgggc cgtgtgaggc cagtgtgcgc   1080
tactcggagc ctctcacgg actgaccgc accagtgtga cagtgagcga cctggagccc   1140
cacatgaact acaccttcac cgtggaggcc cgcaatggcg tctcaggcct ggtaaccagc   1200
cgcagcttcc gtactgccag tgtcagcatc aaccagacag agcccccaa ggtgaggctg   1260
gagggccgca gcaccacctc gcttagcgtc tcttgagca tcccccgcc gcagcagagc   1320
cgagtgtgga agtacgaggt cacttaccgc aagaaggag actccaacag ctacaatgtg   1380
cgccgcaccg agggtttctc cgtgaccctg gacgacctgg cccagacac cacctacctg   1440
gtccagggtc aggcactgac gcaggagggc cagggggccg gcagcagggt gcacgaattc   1500
cagacg                                           1506

```

<210> 22

<211> 1506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human sequence optimized for codon usage in *Listeria*

<400> 22

```

caaggtaaag aagttgtttt attagatttt gcagcagcag gtggtgaatt aggttggtta    60
acacatccat atggtaaagg ttgggattta atgcaaaata ttatgaatga tatgccaatt    120
tatatgtata gtgtttgtaa tgttatgagt ggtgatcaag ataattgggt acgtacaaat    180
tgggtttata gtggtgaagc agaacgtatt tttattgaat taaaatttac agttcgtgat    240
tgtaatatgt ttccagggtg tgcaagtagt tgtaaagaaa catttaattt atattatgca    300
gaaagtgatt tagattatgg tacaaatttt caaaaacgtt tatttacaaa aattgatata    360
attgcaccag atgaaattac agttagtagt gattttgaag cacgtcatgt taaattaaat    420
gttgaagaac gtagtgttgg tccattaaca cgtaaagggt tttatttagc atttcaagat    480
attggtgcat gtgttgcat attaatgtgt cgtgtttatt ataaaaaatg tccagaatta    540

```

```

ttacaagggtt tagcacattt tccagaaaca attgcaggta gtgatgcacc aagtttagca      600
acagttgcag gtacatgtgt tgatcatgca gttgttccac caggtggtga agaaccacgt      660
atgcattgtg cagttgatgg tgaatgggta gttccaattg gtcaatgttt atgtcaagca      720
ggttatgaaa aagttgaaga tgcatgtcaa gcatgtagtc caggtttttt taaatttgaa      780
gcaagtgaaa gtccatgttt agaatgtcca gaacatacat taccaagtcc agaagggtgca      840
acaagttgtg aatgtgaaga aggttttttt cgtgcaccac aagatccagc aagtatgcca      900
tgtacacgtc caccaagtgc accacattat ttaacagcag ttggtatggg tgcaaaagtt      960
gaattacgtt ggacaccacc acaagatagt ggtggtcgtg aagatattgt ttatagtgtt    1020
acatgtgaac aatgttggcc agaaagtggg gaatgtggtc catgtgaagc aagtgttcgt    1080
tatagtgaac caccacatgg tttaacacgt acaagtgtta cagttagtga tttagaacca    1140
catatgaatt atacatttac agttgaagca cgtaatgggtg ttagtggttt agttacaagt    1200
cgtagttttc gtacagcaag tgttagtatt aatcaaacag aaccaccaa agttcgttta    1260

gaaggtcgta gtacaacaag tttaagtgtt agttggagta ttccaccacc acaacaaagt    1320
cgtgttttga aatatgaagt tacatatcgt aaaaaagggtg atagtaatag ttataatgtt    1380
cgtcgtacag aagggttttag tgttacatta gatgatttag caccagatac aacatattta    1440
gttcaagttc aagcattaac acaagaagggt caagggtgcag gtagtcgtgt tcatgaattt    1500
caaaca                                           1506

```

<210> 23
 <211> 502
 <212> PRT
 <213> Homo sapeins

<400> 23

Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu
 1 5 10 15

Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln
 20 25 30

Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val
 35 40 45

Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg
 50 55 60

Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp

65					70					75				80			
Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	Lys	Glu	Thr	Phe	Asn		
				85					90					95			
Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	Thr	Asn	Phe	Gln	Lys		
			100					105					110				
Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	Asp	Glu	Ile	Thr	Val		
		115					120					125					
Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	Glu	Glu	Arg		
	130					135					140						
Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp		
145					150					155					160		
Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys		
				165					170					175			
Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu	Thr	Ile	Ala		
			180					185					190				
Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr	Cys	Val	Asp		
		195					200					205					
His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met	His	Cys	Ala		
	210					215					220						
Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala		
225					230					235					240		
Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe		
				245					250					255			
Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys	Pro	Glu	His		
			260					265					270				
Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly		
		275					280					285					
Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro		
	290					295					300						
Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly	Ala	Lys	Val		
305					310					315					320		

Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile
 325 330 335

Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys
 340 345 350

Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu
 355 360 365

Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr
 370 375 380

Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser
 385 390 395 400

Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro
 405 410 415

Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp
 420 425 430

Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr
 435 440 445

Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu
 450 455 460

Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu
 465 470 475 480

Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg
 485 490 495

Val His Glu Phe Gln Thr
 500

<210> 24
 <211> 1689
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 24
 atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

```

caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180
gagcagggca aggaagtggg actgctggac tttgctgcag ctggagggga gctcggttgg 240
ctcacacacc cgtatggcaa aggggtgggac ctgatgcaga acatcatgaa tgacatgccg 300
atctacatgt actccgtgtg caacgtgatg tctggcgacc aggacaactg gctccgcacc 360
aactgggtgt accgaggaga ggctgagcgt atcttcattg agctcaagtt tactgtacgt 420
gactgcaaca gcttccttgg tggcgccagc tcctgcaagg agactttcaa cctctaactat 480
gccgagtcgg acctggacta cggcaccaac ttccagaagc gcctgttcac caagattgac 540
accattgcgc ccgatgagat caccgtcagc agcgacttcg aggcacgcca cgtgaagctg 600
aacgtggagg agcgctccgt ggggcccgtc acccgcaaag gcttctacct ggccttcacg 660
gatatcgggtg cctgtgtggc gctgctctcc gtccgtgtct actacaagaa gtgccccgag 720
ctgctgcagg gcctggccca cttccctgag accatcgccg gctctgatgc accttccttg 780
gccactgtgg ccggcacctg tgtggaccat gccgtggtgc caccgggggg tgaagagccc 840
cgtatgcact gtgcagtgga tggcgagtgg ctggtgcccc ttgggcagtg cctgtgccag 900
gcaggctacg agaaggtgga ggatgcctgc caggcctgct cgctggatt ttttaagttt 960
gaggcatctg agagccccctg cttggagtgc cctgagcaca cgctgccatc ccctgagggg 1020
gccacctcct gcgagtgtga ggaaggcttc ttccgggcac ctgaggacc agcgctcgatg 1080
ccttgcacac gacccccctc cggcccacac tacctcacag ccgtgggcat ggggtgccaa 1140
gtggagctgc gctggacgcc cctcaggac agcggggggc gcgaggacat tgtctacagc 1200
gtcacctgcg aacagtgtgt gcccgagtct ggggaatgcg ggccgtgtga ggccagtgtg 1260
cgctactcgg agcctcctca cggactgacc cgcaccagtg tgacagtgag cgacctggag 1320
ccccacatga actacacctt caccgtggag gcccgcaatg gcgtctcagg cctggtaacc 1380
agccgcagct tccgtactgc cagtgtcagc atcaaccaga cagagcccc caaggtgagg 1440
ctggagggcc gcagcaccac ctgccttagc gtctcctgga gcatcccccc gccgcagcag 1500
agccgagtgt ggaagtacga ggtcacttac cgcaagaagg gagactccaa cagctacaat 1560
gtgcgccgca ccgaggggtt ctccgtgacc ctggacgacc tggccccaga caccacctac 1620
ctgggtccagg tgcaggcact gacgcaggag ggccaggggg ccggcagcag ggtgcacgaa 1680
ttccagacg

```

<210> 25

<211> 563

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 25

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Gln Gly Lys
 50 55 60

Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp
 65 70 75 80

Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met
 85 90 95

Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
 100 105 110

Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala
 115 120 125

Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser
 130 135 140

Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr
 145 150 155 160

Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe
 165 170 175

Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp
 180 185 190

Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly
 195 200 205

Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala
 210 215 220

Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu
 225 230 235 240

Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp
 245 250 255

Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala Val
 260 265 270

Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp Gly
 275 280 285

Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu
 290 295 300

Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe
 305 310 315 320

Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro
 325 330 335

Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg
 340 345 350

Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala
 355 360 365

Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg
 370 375 380

Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser
 385 390 395 400

Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys
 405 410 415

Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr
 420 425 430

Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr
 435 440 445

Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe
 450 455 460

Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg
465 470 475 480

Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro
485 490 495

Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys
500 505 510

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser
515 520 525

Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val
530 535 540

Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His Glu
545 550 555 560

Phe Gln Thr

<210> 26
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein construct

<400> 26
ggtacctcct ttgattagta tttcctatc ttaaagttac ttttatgtgg aggcattaac 60
atgtgtaaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
atattgcgtt tcattcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
aaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa 300
actgaagcaa aggatgcac tgcattcaat aaagaaaatt caatttcac catggcacca 360
ccagcatctc cgcttgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc 420
gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttcagca 480

gcaggtggtg aattaggttg gttaacacat ccatatggta aaggttggga tttaatgcaa 540
aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagggtgat 600
caagataatt ggttacgtac aaattgggtt tatcgtggtg aagcagaacg tatttttatt 660

```

gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840
gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900
ggtttttatt tagcatttca agatattggg gcatgtgttg cattattaag tgttcgtggt 960
tattataaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca 1020
ggtagtgatg caccaagttt agcaacagtt gcaggtagat gtgttgatca tgcagttggt 1080
ccaccagggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca 1140
attgggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt 1200
agtccagggt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat 1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca 1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca 1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtggtggt 1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tgggtgaatgt 1500
gggccatgtg aagcaagtgt tcgttatagt gaaccaccac atggtttaac acgtacaagt 1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat 1620
gggtgtagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa 1680
acagaaccac caaaagttcg tttagaagggt cgtagtacia caagtttaag tgtaggttg 1740
agtattccac caccacaaca aagtcgtggt tggaaatatg aagttacata tcgtaaaaaa 1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtggtac attagatgat 1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaagggt 1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta 1980
tgagagctc 1989

```

<210> 27

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 27

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10           15

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
 50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala
 65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly
 85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr
 100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr
 115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys
 130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys
 145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly
 165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro
 180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu
 195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr
 210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg
 225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe
 245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala
 260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro
 275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp

500

505

510

Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn
 515 520 525

Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro
 530 535 540

Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln
 545 550 555 560

Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile
 565 570 575

Ser Glu Glu Asp Leu
 580

<210> 28
 <211> 1989
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct for fusion protein

<400> 28
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
 aaaaaaatta tgttagtttt tattacatta attttagtta gtttaccaat tgcacaacaa 300
 acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtattagtag tatggcacca 360
 ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420
 gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttgcagca 480
 gcaggtggtg aattaggttg gttaacacat ccatatggta aagggtggga tttaatgcaa 540
 aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtggatgat 600
 caagataatt ggttacgtac aaattgggtt tatcgtggtg aagcagaacg tatttttatt 660
 gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720
 gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780
 cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840
 gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900

```

ggtttttatt tagcatttca agatattggt gcatgtgttg cattattaag tgttcgtggt      960
tattataaaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca    1020
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgatca tgcagttggt    1080
ccaccagggtg gtgaagaacc acgtatgcat tgtgcagttg atgggtgaatg gttagttcca    1140
attgggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt    1200
agtccagggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat    1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca    1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca    1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtggtggt    1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tgggtgaatgt    1500
ggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atggtttaac acgtacaagt    1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat    1620
ggtgttagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa    1680
acagaaccac caaaagttcg tttagaaggt cgtagtacaa caagtttaag tgttagttgg    1740
agtattccac caccacaaca aagtcgtggt tggaaatatg aagttacata tcgtaaaaaa    1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtgttac attagatgat    1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaagggt    1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta    1980
tgagagctc                                     1989

```

<210> 29

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion protein

<400> 29

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10          15

```

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20          25          30

```

```

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35          40          45

```


Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
 50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala
 65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly
 85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr
 100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr
 115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys
 130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys
 145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly
 165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro
 180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu
 195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr
 210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg
 225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe
 245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala
 260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro
 275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp
 500 505 510

Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn
 515 520 525

Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro
 530 535 540

Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln
 545 550 555 560

Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile
 565 570 575

Ser Glu Glu Asp Leu
 580

<210> 30
 <211> 1968
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 30
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattagggtt aaaaaatgta gaaggagagt gaaacccatg 240
 gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300
 aatacgtttg accgcgcgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360
 ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420
 aaacaaggta aagaagttgt tttattagat tttgcagcag caggtggtga attaggttgg 480
 ttaacacatc catatggtaa aggttgggat ttaatgcaa atattatgaa tgatatgcca 540
 atttatatgt atagtgtttg taatgttatg agtggatgac aagataattg gttacgtaca 600
 aattgggttt atcgtggtga agcagaacgt atttttattg aattaaaatt tacagttcgt 660
 gattgtaata gttttccagg tgggtgcaagt agttgtaaag aaacatttaa tttatattat 720
 gcagaaagtg atttagatta tgggtacaaat tttcaaaaac gtttatttac aaaaattgat 780
 acaattgcac cagatgaaat tacagttagt agtgattttg aagcacgtca tggttaaatta 840
 aatgttgaag aacgtagtgt tgggtccatta acacgtaaag gtttttattt agcatttcaa 900
 gatattggtg catgtgttgc attattaagt gttcgtgttt attataaaaa atgtccagaa 960
 ttattacaag gtttagcaca ttttccagaa acaattgcag gtagtgatgc accaagttta 1020
 gcaacagttg caggtacatg tgttgatcat gcagttgttc caccaggtgg tgaagaacca 1080

```

cgtatgcatt gtgcagttga tggatgaatgg ttagttccaa ttgggtcaatg tttatgtcaa 1140
gcagggttatg aaaaagttga agatgcatgt caagcatgta gtccagggtt ttttaaattt 1200
gaagcaagtg aaagtccatg tttagaatgt ccagaacata cattaccaag tccagaaggt 1260
gcaacaagtt gtgaatgtga agaagggttt tttcgtgcac cacaagatcc agcaagtatg 1320
ccatgtacac gtccaccaag tgcaccacat tatttaacag cagttggtat ggggtgcaaaa 1380
gttgaattac gttggacacc accacaagat agtggtggtc gtgaagatat tgtttatagt 1440
gttacatgtg aacaatgttg gccagaaagt ggtgaatgtg gtccatgtga agcaagtgtt 1500
cgttatagtg aaccaccaca tggtttaaca cgtacaagtg ttacagttag tgatttagaa 1560
ccacatatga attatacatt tacagttgaa gcacgtaatg gtgtagtggt tttagttaca 1620
agtcgtagtt ttcgtacagc aagtgttagt attaatacaa cagaaccacc aaaagttcgt 1680
ttagaagggtc gtagtacaac aagtttaagt gttagttgga gtattccacc accacaacaa 1740
agtcgtgttt ggaaatatga agttacatat cgtaaaaaag gtgatagtaa tagttataat 1800
gttcgtcgta cagaagggtt tagtgttaca ttagatgatt tagcaccaga tacaacatat 1860
ttagttcaag ttcaagcatt aacacaagaa ggtcaagggt caggtagtcg tgttcatgaa 1920
tttcaaacag aacaaaaatt aattagttaa gaagatttat gagagctc 1968

```

<210> 31

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 31

```

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10           15

```

```

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly
          20           25           30

```

```

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser
          35           40           45

```

```

Val Gly Ala Phe Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gln Gly
          50           55           60

```

```

Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly
65           70           75           80

```

Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile
85 90 95

Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser
100 105 110

Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu
115 120 125

Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn
130 135 140

Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr
145 150 155 160

Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu
165 170 175

Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser
180 185 190

Asp Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val
195 200 205

Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly
210 215 220

Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro
225 230 235 240

Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser
245 250 255

Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala
260 265 270

Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp
275 280 285

Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr
290 295 300

Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys
305 310 315 320

-38-

565

570

<210> 32
 <211> 1254
 <212> DNA
 <213> Homo sapiens

<400> 32
 caccgcagga ggaagaacca gcgtgcccgc cagtccccgg aggacgttta cttctccaag 60
 tcagaacaac tgaagcccct gaagacatac gtggaccccc acacatatga ggaccccaac 120
 caggctgtgt tgaagttcac taccgagatc catccatcct gtgtcactcg gcagaagggtg 180
 atcggagcag gagagtttgg ggagggtgtac aaggggcatgc tgaagacatc ctcggggaag 240
 aaggaggtgc cgggtggccat caagacgctg aaagccggct acacagagaa gcagcgagtgc 300
 gacttcctcg gcgaggcccg catcatgggc cagttcagcc accacaacat catccgccta 360
 gagggcgctca tctccaaata caagcccatg atgatcatca ctgagtacat ggagaatggg 420
 gccctggaca agttccttcg ggagaaggat ggcgagttca gcgtgctgca gctggtgggc 480
 atgctgcggg gcatcgagc tggcatgaag tacctggcca acatgaacta tgtgcaccgt 540
 gacctggctg cccgcaacat cctcgtcaac agcaacctgg tctgcaaggt gtctgacttt 600
 ggctgtccc gcgtgctgga ggacgacccc gagggcacct acaccaccag tggcggcaag 660
 atccccatcc gctggaccgc cccggaggcc atttcctacc ggaagttcac ctctgccagc 720
 gacgtgtgga gctttggcat tgtcatgttg gaggtgatga cctatggcga gcggccctac 780
 tgggagttgt ccaaccacga ggtgatgaaa gccatcaatg atggcttcg gctccccaca 840
 cccatggact gccctccgc catctaccag ctcatgatgc agtgctggca gcaggagcgt 900
 gcccgcgcgc ccaagttcgc tgacatcgtc agcatcctgg acaagctcat tcgtgcccct 960
 gactccctca agaccctggc tgactttgac ccccgctgt ctatccggct cccagcacg 1020
 agcggctcgg agggggtgcc cttccgcacg gtgtccgagt ggctggagtc catcaagatg 1080
 cagcagtata cggagcactt catggcggcc ggctacactg ccatcgagaa ggtggtgcag 1140
 atgaccaacg acgacatcaa gaggattggg gtgcggctgc ccggccacca gaagcgcac 1200
 gcctacagcc tgctgggact caaggaccag gtgaacactg tggggatccc catc 1254

<210> 33
 <211> 1254
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sequence Optimized for codon usage in Listeria

<400> 33
cacagacgta gaaaaaatca acgtgctcga caatccccag aagatgtgta tttttcgaaa 60
agtgaacaat taaaaccatt aaaaacttat gttgatccgc atacgtacga agacccaaatt 120
caagcagtat taaaatttac aacagaaata caccgaagtt gtgttacaag acaaaaagtt 180
attggagcag gtgaattcgg agaggatatat aaaggatatgt taaaaacatc atcaggtaaa 240
aaagaagttc cggttgcaat taaaacctta aaggcaggat atacagaaaa acagcgagtt 300
gatttttttag gtgaagcagg aattatgggt caatttagcc atcataatat tattcgtttg 360
gaaggagtaa taagtaaata taaaccaatg atgattatta cagaatacat ggaaaacggt 420
gcttttagata aattttttacg tgaaaaggat ggtgaattta gtgttttaca attgggttggt 480
atgttaagag gaattgctgc aggtatgaaa tatttagcta atatgaatta tgttcaccgt 540
gatttggcag caagaaatat cctagtcaat tccaatttag tatgtaaagt tagtgatttt 600
ggtttaagca gagtattaga agacgatcca gaggcaacct atacaacatc gggaggtaaa 660
attcctattc gttggacagc accagaagct atcagttacc gtaaatttac aagtgcacat 720
gacgtgtgga gttttgggat tgtaatgtgg gaagttatga catatggaga aagaccatat 780
tggaattaa gtaatcatga agttatgaaa gcaattaacg atggatttag attaccaact 840
ccgatggatt gtccatctgc catttatcaa ctaatgatgc aatgttggca acaagaaaga 900
gcacgacgtc caaaatttgc agatattggt agtatttttag acaaattaat tcgtgcacca 960
gatagtttaa aaacttttagc agactttgat cctcgtgtta gtattcgatt accaagtacg 1020
tcaggttccg aaggagttcc atttcgcaca gtctccgaat ggttggaatc aattaaatg 1080
caacaatata ccgaacactt tatggcagca gggtacacag caatcgaaaa agttgttcaa 1140
atgacaaaatg atgatattaa acgtattgga gtttagattac caggccacca gaaacgtatt 1200
gcatattctt tattaggttt aaaagatcaa gttaataccg tgggaattcc aatt 1254

<210> 34
<211> 456
<212> PRT
<213> Homo sapiens

<400> 34

Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala
1 5 10 15

Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala
20 25 30

Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala Arg
35 40 45

Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro
 50 55 60

Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala
 65 70 75 80

Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln
 85 90 95

Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu
 100 105 110

Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu
 115 120 125

Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala
 130 135 140

Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly
 145 150 155 160

Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu
 165 170 175

Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser
 180 185 190

Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys
 195 200 205

Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn
 210 215 220

Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu
 225 230 235 240

Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly
 245 250 255

Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg
 260 265 270

Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp
 275 280 285

Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His
 290 295 300

Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met
 305 310 315 320

Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln
 325 330 335

Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp
 340 345 350

Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp
 355 360 365

Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val
 370 375 380

Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln
 385 390 395 400

Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val
 405 410 415

Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro
 420 425 430

Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln
 435 440 445

Val Asn Thr Val Gly Ile Pro Ile
 450 455

<210> 35

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein

<400> 35

atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120

ccaccagcat ctccgctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180

```

gagcaccgca ggaggaagaa ccagcgtgcc cgccagtccc cggaggacgt ttacttctcc 240
aagtcagaac aactgaagcc cctgaagaca tacgtggacc cccacacata tgaggacccc 300
aaccaggctg tgttgaagtt cactaccgag atccatccat cctgtgtcac tcggcagaag 360
gtgatcggag caggagagtt tggggagggtg tacaagggca tgctgaagac atcctcgggg 420
aagaaggagg tgccggtggc catcaagacg ctgaaagccg gctacacaga gaagcagcga 480
gtggacttcc tcggcgaggc cggcatcatg ggccagtcca gccaccacaa catcatccgc 540
ctagagggcg tcatctccaa atacaagccc atgatgatca tcaactgagta catggagaat 600
ggggccctgg acaagttcct tcgggagaag gatggcgagt tcagcgtgct gcagctgggtg 660
ggcatgctgc ggggcatcgc agctggcatg aagtacctgg ccaacatgaa ctatgtgcac 720
cgtgacctgg ctgcccgcaa catcctcgtc aacagcaacc tggctctgaa ggtgtctgac 780
tttggcctgt cccgcgtgct ggaggacgac cccgaggcca cctacaccac cagtggcggc 840

aagatcccca tccgctggac cgccccggag gccatttcct accggaagtt cacctctgcc 900
agcgacgtgt ggagctttgg cattgtcatg tgggaggtga tgacctatgg cgagcggccc 960
tactgggagt tgtccaacca cgaggtgatg aaagccatca atgatggctt ccggctcccc 1020
acacccatgg actgcccctc cgccatctac cagctcatga tgcagtgtg gcagcaggag 1080
cgtgccccgc gccccaagtt cgctgacatc gtcagcatcc tggacaagct cattcgtgcc 1140
cctgactccc tcaagaccct ggctgacttt gacccccgcg tgtctatccg gctccccagc 1200
acgagcggct cggaggggggt gcccttcgc acggtgtccg agtggctgga gtccatcaag 1260
atgcagcagt atacggagca cttcatggcg gccggctaca ctgccatcga gaaggtgggtg 1320
cagatgacca acgacgacat caagaggatt ggggtgcggc tgcccggcca ccagaagcgc 1380
atcgcttaca gcctgctggg actcaaggac caggtgaaca ctgtggggat ccccatc 1437

```

<210> 36

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Protein Sequence

<400> 36

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10           15

```

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20           25           30

```

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu His Arg Arg
 50 55 60

Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser
 65 70 75 80

Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr
 85 90 95

Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His
 100 105 110

Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly
 115 120 125

Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val
 130 135 140

Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg
 145 150 155 160

Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His
 165 170 175

Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met
 180 185 190

Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg
 195 200 205

Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg
 210 215 220

Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His
 225 230 235 240

Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys
 245 250 255

Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu
 260 265 270

Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala
 275 280 285

Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp
 290 295 300

Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro
 305 310 315 320

Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly
 325 330 335

Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu
 340 345 350

Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala
 355 360 365

Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu
 370 375 380

Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser
 385 390 395 400

Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu
 405 410 415

Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly
 420 425 430

Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys
 435 440 445

Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser
 450 455 460

Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 465 470 475

<210> 37

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein sequence

<400> 37

ggtacctcct ttgattagta ttttcctatc ttaaagttac ttttatgtgg aggcattaac	60
at ttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcggt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg	180
gtggcaaacg gtatttggca ttattagggt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa	300
actgaagcaa aggatgcac tgcattcaat aaagaaaatt caatttcac catggcacca	360
ccagcatctc cgctgcaag tctaagacg ccaatcgaaa agaaacacgc ggatggatcc	420
gattataaag atgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc	480
ccagaagatg tgtatttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat	540
ccgcatacgt acgaagaccc aaatcaagca gtattaaaat ttacaacaga aatacaccca	600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaaggt	660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca	720
ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggatcaattt	780
agccatcata atattattcg ttggaagga gtaataagta aatataaacc aatgatgatt	840
attacagaat acatggaaaa cggtgcttta gataaatttt tacgtgaaaa ggatggtgaa	900
tttagtgttt tacaattggg tggtatgtta agaggaattg ctgcaggtat gaaatattta	960
gctaatatga attatgttca ccgtgatttg gcagcaagaa atatcctagt caattccaat	1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1080
acctatacaa catcgggagg taaaattcct attcgttgga cagcaccaga agctatcagt	1140
taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt	1380
ttagacaaat taattcgtgc accagatagt ttaaaaaactt tagcagactt tgatcctcgt	1440
gtagtatc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatgggttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaacgtat tggagttaga	1620
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat	1680
accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc	1737

<210> 38

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 38

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
 50 55 60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln
 65 70 75 80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu
 85 90 95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val
 100 105 110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys
 115 120 125

Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys
 130 135 140

Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys
 145 150 155 160

Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly
 165 170 175

Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val
 180 185 190

Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn
 195 200 205

Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val
 210 215 220

Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr
 225 230 235 240

Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 245 250 255

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser
 260 265 270

Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly
 275 280 285

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys
 290 295 300

Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu
 305 310 315 320

Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu
 325 330 335

Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp
 340 345 350

Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu
 355 360 365

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
 370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro
 385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro
 405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr
 420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val
 435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly

450	455	460
His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val		
465	470	475 480
Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp		
	485	490 495

Leu

<210> 39
 <211> 1737
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 39
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcggtt tcattcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaaacg gtatttggca ttattagggtt aaaaaatgta gaaggagagt gaaacccatg 240
 aaaaaaatta tgtagttttt tattacatta atttttagtta gtttaccat tgcacaacaa 300
 acagaagcaa aagatgcaag tgcattttaat aaagaaaata gtattagtag tatggcacca 360
 ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420
 gattataaag acgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc 480
 ccagaagatg tgtattttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat 540
 ccgcatacgt acgaagaccc aaatcaagca gtattaaaat ttacaacaga aatacaccca 600
 agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaagg 660
 atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca 720
 ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggatcaattt 780
 agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt 840
 attacagaat acatggaaaa cgggtgcttta gataaatttt tacgtgaaaa ggatgggtgaa 900
 tttagtgttt tacaattgggt tggtatgtta agaggaattg ctgcaggtat gaaatattta 960
 gctaatatga attatgttca ccgtgatttg gcagcaagaa atatcctagt caattccaat 1020
 ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca 1080
 acctatacaa catcgggagg taaaattcct attcgttgga cagcaccaga agctatcagt 1140

taccgtaa at ttacaagtgc atcagacgtg tggagttttg ggattgta at gtgggaagtt 1200
 atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt 1260
 aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg 1320
 atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt 1380
 ttagacaaat taattcgtgc accagatagt ttaaaaactt tagcagactt tgatcctcgt 1440
 gttagtattc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc 1500
 gaatggttgg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac 1560
 acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaacgtat tggagttaga 1620
 ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat 1680
 accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc 1737

<210> 40
 <211> 497
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 40

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
 50 55 60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln
 65 70 75 80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu
 85 90 95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val
 100 105 110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys

115	120	125
Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys 130 135 140		
Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys 145 150 155 160		
Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly 165 170 175		
Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val 180 185 190		
Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn 195 200 205		
Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val 210 215 220		
Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr 225 230 235 240		
Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 245 250 255		
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser 260 265 270		
Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly 275 280 285		
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys 290 295 300		
Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu 305 310 315 320		
Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu 325 330 335		
Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp 340 345 350		
Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu 355 360 365		

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
 370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro
 385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro
 405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr
 420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val
 435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly
 450 455 460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val
 465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp
 485 490 495

Leu

<210> 41
 <211> 1716
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 41
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
 gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300
 aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360
 ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420

```

aaacacagac gtagaaaaaa tcaacgtgct cgacaatccc cagaagatgt gtatTTTTcg      480
aaaagtgaac aattaaaacc attaaaaact tatgttgatc cgcatacgta cgaagaccca      540
aatcaagcag tattaaaatt tacaacagaa atacacccaa gttgtgttac aagacaaaaa      600
gttattggag caggtgaatt cggagaggta tataaaggta tgttaaaaac atcatcaggt      660
aaaaaagaag ttccggttgc aattaaaacc ttaaaggcag gatatacaga aaaacagcga      720
gttgatTTTT taggtgaagc aggaattatg ggtcaattta gccatcataa tattattcgt      780
ttggaaggag taataagtaa atataaacca atgatgatta ttacagaata catggaaaac      840
ggtgcttttag ataaatTTTT acgtgaaaag gatggtgaat ttagtgTTTT acaattgggt      900
ggtatgTTaa gaggaattgc tgcaggatg aaatatTTtag ctaatatgaa ttatgttcac      960
cgtgatttgg cagcaagaaa tatcctagtc aattccaatt tagtatgtaa agttagtgat     1020
tttggtTTaa gcagagtatt agaagacgat ccagaggcaa cctatacaac atcggggagg      1080
aaaattccta ttcgttggac agcaccagaa gctatcagtt accgtaaatt tacaagtgca     1140
tcagacgtgt ggagttttgg gattgtaatg tgggaagtta tgacatatgg agaaagacca     1200
tattgggaat taagtaatca tgaagttatg aaagcaatta acgatggatt tagattacca     1260
actccgatgg attgtccatc tgccatttat caactaatga tgcaatgttg gcaacaagaa     1320
agagcacgac gtccaaaatt tgcagatatt gttagtattt tagacaaatt aattcgtgca     1380
ccagatagtt taaaaacttt agcagacttt gatcctcgtg ttagtattcg attaccaagt     1440
acgtcaggtt ccgaaggagt tccatttcgc acagtctccg aatggttgga atcaattaaa     1500
atgcaacaat acaccgaaca ctttatggca gcaggttaca cagcaatcga aaaagttggt     1560
caaatgacaa atgatgatat taaacgtatt ggagttagat taccaggcca ccagaaacgt     1620
attgcatatt ctttattagg tttaaaagat caagttaata ccgtgggaat tccaattgaa     1680
caaaaattaa ttccgaaga agacttataa gagctc                                1716

```

<210> 42

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 42

```

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10          15

```

```

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly

```

20					25					30					
Ala	Gly	Lys	Ile	Ala	Gly	Leu	Ser	Leu	Gly	Leu	Thr	Ile	Ala	Gln	Ser
		35					40					45			
Val	Gly	Ala	Phe	Gly	Ser	Asp	Tyr	Lys	Asp	Asp	Asp	Lys	His	Arg	
	50					55					60				
Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe
65						70					75				80
Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	Lys	Thr	Tyr	Val	Asp	Pro	His
				85					90					95	
Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile
			100						105					110	
His	Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	Val	Ile	Gly	Ala	Gly	Glu	Phe
			115					120					125		
Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu	Lys	Thr	Ser	Ser	Gly	Lys	Lys	Glu
	130					135					140				
Val	Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln
145						150					155				160
Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	Ile	Met	Gly	Gln	Phe	Ser	His
				165					170					175	
His	Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	Ile	Ser	Lys	Tyr	Lys	Pro	Met
			180					185					190		
Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly	Ala	Leu	Asp	Lys	Phe	Leu
		195					200					205			
Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	Leu	Gln	Leu	Val	Gly	Met	Leu
	210					215					220				
Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val
225						230					235				240
His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val
				245					250					255	
Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro
			260					265					270		

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
 275 280 285

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
 290 295 300

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
 305 310 315 320

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
 325 330 335

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
 340 345 350

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
 355 360 365

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
 370 375 380

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
 385 390 395 400

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
 405 410 415

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
 420 425 430

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
 435 440 445

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
 450 455 460

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 465 470 475 480

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 485 490

<210> 43
 <211> 9808
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein Construct

<400> 43

```

ctttaaacgt ggatcatttt ctttaaattt atgctgacga cctttgaatt tgcctttttt      60
cttagcaatt tcgattcctt gtgcctgacg ttccttaatt ttttttcggt ctgattctgc      120
ttgatacttg tacaattcaa tgacaaggct attaatcaaa cgccttaaatt tttcatcttc      180
aataccattc attgagggta aatttaagac ttccagggtt gcccccttaa tttgaatttg      240
attcatcaat tctgttaatt ctttattatt tcgtcctaatt cgatctaatt cagtaacaat      300
aacaatatcc ccttcacgaa tatagttaag catagcttgt aattgtgggc gttcgaccga      360
ttgaccgctt aatttgtctg aaaagacctt agaaacgccc tgtaacgctt gtaattgccg      420
atctaagttc tgttctttgc tactgacacg tgcataacca attttagcca ttttcaacca      480
acctctaaaa ttctctcggt tgcaataacc aatcagcaat atctactttt tcaatttcaa      540
attgcttata agaaattgtc ttttcgtaag cgataaaaac ttgcgcataat tgttgctcat      600
taaaaatagc caccacttcg tcattttcta aaactcgata aataaatttt ttcattttac      660
tcctcctatt atgcccact taaatgacct attcaccaag tcaattatac tgctaaaac      720
atattaggac aaataggtat actctattga cctataaatg atagcaactt aaaagatcaa      780
gtgttcgctt cgctctcact gcccctcgac gttttagtag cctttccctc acttcggtca      840
gtccaagcca actaaaagtt ttggggctac tctctccttc tccccctaat aattaattaa      900
aatcttactc tgtatatattc tgctaatacat tcactaaaca gcaaagaaaa acaaacacgt      960
atcatagata taaatgtaat ggcatagtgcc gggttttatt ttcagcctgt atcgtagcta      1020
aacaaatcga gttgtgggtc cgttttgggg cgttctgcca atttgttttag agtttcttga      1080
ataaatgtac gttctaaatt aaacgaagct gtcagcgctt ttatatagct ttctcggttct      1140
tcttttttta atttaatgat cgatagcaac aatgatttaa cactagcaag ttgaatgcca      1200
ccatttcttc ctggtttaat cttaaagaaa atttcctgat tcgccttcag taccttcagc      1260
aatttatcta atgtccgttc aggaatgcct agcacttctc taatctcttt tttggtcgctc      1320
gctaaataag gcttgtatac atcgcttttt tcgctaatat aagccattaa atcttctttc      1380
cattctgaca aatgaacacg ttgacgttcg cttctttttt tcttgaattt aaaccaccct      1440
tgacggacaa ataaatcttt actggttaaa tcacttgata cccaagcttt gcaaagaatg      1500
gtaatgtatt ccctattagc cccttgatag ttttctgaat aggcacttct aacaattttg      1560
attacttctt tttcttctaa gggttgatct aatcgattat taaactcaaa catattatat      1620
tcgcacgttt cgattgaata gcctgaacta aagtaggcta aagagagggt aaacataacg      1680

```


ctattgcgcc	ctactaaacc	cttttctcct	gaaaatttcg	tttcgtgcaa	taagagatta	1740
aaccaggggt	catctacttg	ttttttgcct	tctgtaccgc	ttaaaaccgt	tagacttgaa	1800
cgagtaaagc	ccttattatc	tgtttggttg	aaagaccaat	cttgccattc	tttgaaagaa	1860
taacggtaat	tgggatcaaa	aaattctaca	ttgtccgttc	ttggtatacg	agcaatccca	1920
aaatgattgc	acgttagatc	aactggcaaa	gactttccaa	aatattctcg	gatattttgc	1980
gagattat	ttt	tggtgcttt	gacagattta	aattctgatt	ttgaagtcac	2040
gtttctaaaa	caaaatatgc	ttgataacct	ttatcagatt	tgataattaa	cgtaggcata	2100
aaacctaaat	caatagctgt	tgttaaaata	tcgcttgctg	aaatagtttc	tttttccgtg	2160
tgaatatcaa	aatcaataaa	gaaggatttg	atgtgtctta	aattgttttc	agaatgtcct	2220
ttagtgtatg	aacggttttc	gtctgcatac	gtaccataac	gataaacggt	tggtgtccaa	2280
tgcgtaaagt	tatcttgatt	ttcgtgaatc	gcttcttcgg	aagtcagaac	aacgccacgt	2340
ccgccaatca	tgcttttttt	tgagcgatac	gcaaaaatag	cccctttact	tttacctggc	2400
ttggtagtga	ttgagcgaat	tttactat	tt	aaattt	gt	2460
agcacagttt	ctacaacaaa	agggatattc	attcagctgt	tctcctttct	tacgaaaatt	2520
aattagttag	aagctacgat	caaagttgaa	tcacaacaaa	aaaggcaatc	aactaagttt	2580
ttcttaattg	attgcttggg	atcttcttaa	agacttgaaa	tcccctcaaa	aacccgatat	2640
aatgggttta	cagatat	tt	agtatctgat	taataaagta	attaaatact	2700
ttgggtctcg	acttctttta	ttgattgggtg	gtaatcaatt	aaggctcgca	gttaaaat	2760
ctcaggcttt	aactggctcg	ggctcttttt	ttgtattctt	tattcagttc	gttgtttcgt	2820
tatatctagt	atatcgcttt	ttaaaaaat	aagcaatgat	ttcgtgcatt	attcacacga	2880
aatcattgct	tttttcttct	tccatttcta	actccaatgt	tacttgttct	gtttctgggt	2940
ctggttctgt	tggtcattt	gggattaaat	ccactactag	cgttgagtta	gttccgtctc	3000
taatagccgg	ttaagtaata	gccgggtaag	tggtcaaact	ttgggaaaat	ctcaaccgc	3060
attaagtttt	gatgccatga	caatcgttgg	aaatttgaac	aaaactaatg	ctaaaaagct	3120
atctgacttt	atgagtgtag	agccacaaat	acgactttgg	gatatacttc	aaacaaagtt	3180
taaagctaag	gcacttcaag	aaaaagttta	tatcgaatat	gacaaagtaa	aagcagatac	3240
ttgggataga	cgtaatatgc	gtgttggaatt	taatcccaat	aaactcacac	atgaagaaat	3300
gatttggtta	aaacaaaata	ttatcgacta	catggaagat	gacggtttta	caagattaga	3360
cttagctttt	gattttgaag	atgatttgag	cgattactat	gcaatgactg	ataaagcagt	3420
taagaaaact	gttttttatg	gtcgtaatgg	caagccagaa	acaaaatatt	ttggtgtccg	3480

tgatagtgat	agattttatta	gaattttataa	taaaaaaciaa	gaacgtaaag	ataacgcaga	3540
tgttgaagtt	gtgtttgaac	atttatggcg	tgtagaagtt	gaattaaaaa	gagatatggt	3600
tgattactgg	aatgattggt	ttaatgattt	acacatcttt	gaaacctgcg	tggtgctactt	3660
tagaaaaaat	taatgagcaa	gctatgggtt	atactttggt	gcatgaagaa	agtatgtggg	3720
gaaagctaag	taagaatact	aagactaaat	ttaaaaaatt	gattagagaa	atatctccaa	3780
ttgatttaac	ggaattaatg	aaatcgactt	taaaagcgaa	cgaaaaaciaa	ttgcaaaagc	3840
agattgattt	ttggcaacgt	gaatttaggt	tttggaagta	aaataagttt	tatttgataa	3900
aaattgctaa	ttcagtataa	ttaatattta	cgagggtgaca	taacgtatga	aaaaatcaga	3960
ggattattcc	tcctaaatat	aaaaatttaa	aatttaggag	gaagttatat	atgactttta	4020
atattattga	attagaaaaat	tggtatagaa	aagaatattt	tgaacactat	tttaatcagc	4080
aaactactta	tagcattact	aaagaaattg	atattacttt	gtttaaagat	atgataaaaa	4140
agaaaggata	tgaaatttat	ccctctttta	tttatgcaat	tatggaagtt	gtaaataaaa	4200
ataaagtgtt	tagaacagga	attaatagtg	agaataaatt	aggttattgg	gataagttaa	4260
atcctttgta	tacagttttt	aataagcaaa	ctgaaaaatt	tactaacatt	tggtactgaat	4320
ctgataaaaa	cttcatttct	ttttataata	attataaaaa	tgacttgctt	gaatataaag	4380
ataaagaaga	aatgtttcct	aaaaaaccca	tacctgaaaa	caccataccg	atttcaatga	4440
ttccttggat	tgatttttagt	tcattttaatt	taaatattgg	taacaatagc	agcttttttat	4500
tgcttattat	tacgatagggt	aaattttata	gtgagaataa	taaaatttat	ataccagttg	4560
ctctgcaact	tcattcattct	gtatgtgatg	gttaccatgc	ttcactattt	atgaatgaat	4620
ttcaagatat	aattcatagg	gtagatgatt	ggatttagtt	tttagatttt	gaaagtgaat	4680
ttaattttat	acacgtaagt	gatcataaaa	tttatgaacg	tataacaacc	acatttttttg	4740
gttgcttggt	gtttttgattt	tgaatttggt	tttgaactta	tggtactgatt	tattcagttc	4800
atttttttgtg	cttgccacaaa	aactagcctc	gcagagcaca	cgcattaatg	acttatgaaa	4860
cgtagtaaat	aagtctagtg	tggtatactt	tacttggaag	atgcaccgaa	taaaaaatat	4920
tgaagaaciaa	ctagcaaaaag	atttttaaaga	gttattttat	tttaagtctt	tataacatga	4980
gtgaagcgaa	ttttttaaatt	tcgatagaaa	tttttacatc	aaaaagcccc	ctgtcaaaaat	5040
tgacgaaggg	ggtttttttg	cgcacgcttt	tcgttagaaa	tatacaagat	tgaaaatcgt	5100
gtataagtgc	gccctttggt	ttgaacttag	cacgttacat	caattttttta	aaatgatgta	5160
taagtgcgcc	cttttaaaatt	ttgagtgatt	atatttttttg	agttagaaaa	agggattggg	5220
aaaatttccc	aaaataattt	aaaaaataag	caaaaatttt	cgatagagaa	tgtgctattt	5280
tttgtcaaag	gtgtatacct	tgactgtgct	tgctgttaca	ttaagtttat	ttttaagtta	5340

ttaaaaaaga aatagctttt aaagtttggc tgcgtgtcgc tttataaagc tgattgactt	5400
ttgattgcaa actacttaaa gaaaacaaac teggactatt cgttttcttc tctttggttt	5460
gaacatcagc aattatcccc tcttgattgc ctatttttagc ttgttttagaa gaaacaaaag	5520
ctaaaagctc ctcttgggtt ttaaaacgct gtgtgggggt tagaacgcc ttaaagcacc	5580
cttggttttac ttttatacta gcttccacct cgaaaaaagg ttctttttta aaattctcta	5640
tggcttcttg gcgctgaaaa aataaggat aaggtgggcg tttgaacacg tcctagttaa	5700
aatgtacctt gtacgcccct tctgttgtaa atttaacgta taaaagggc ttgcgttcat	5760
gccgatcaac caatcggcaa tttggcgtgt ttgcgttct tgataaaagg gatagtaatt	5820
cattccaggt tgcaaatttt gaaaaccgct tccgattaca tctttttcta agctattgat	5880
ccatagtctt ttaaagtgtt tatcttttga aaaggcattt gctttatgga taatcgacca	5940
ggcgatattt tcaccttctc tgctgctatc tgttgcaaca ataattgtat ttgccttttt	6000
gagaagttct gcaacaattt taaactgctt tcccttatct tttgcaactt caaaatcgta	6060
tcgatcagga aaaatcggca aagattcaag tttccaattt tgccactttt cgtcataatg	6120
acctggttct gctaattcca ctaaagtccc aaaccaaag gtgataaacg tttcatctgt	6180
aaatagtggg tctttgatct caaaataacc gtcttttttg gtgctttgtt ttaaagcact	6240
tgcgtaggct aatgcctggc ttggtttttc agctaaaata accgtactca ttaactatcc	6300
ctcttttcat tgttttttct ttgatcgact gtcacgttat atcttgctcg ataccttcta	6360
aacgttcggc gattgattcc agtttgttct tcaacttctt tatcggataa accattcaaa	6420
aacaaatcga aagcatggat gcgccgcgtg cggctgctgg agatggcgga cgcgatggat	6480
atgttctgcc aagggttggg ttgcgcattc acagttctcc gcaagaattg attggctcca	6540
attcttgag tggtgaatcc gttagcgagg tgccgccggc ttccattcag gtcgaggtgg	6600
cccggctcca tgcaccgga cgcaacgcgg ggaggcagac aaggtatagg gcggcgctta	6660
caatccatgc caaccggtc catgtgctcg ccgaggcggc ataaatcgcc gtgacgatca	6720
gcgggtccagt gatcgaagtt aggctggtta gagccgcgag cgatccttga agctgtccct	6780
gatggtcgtc atctacctgc ctggacagca tggcctgcaa cgcgggcatc ccgatgccgc	6840
cggaagcgag aagaatcata atggggaagg ccatccagcc tcgcgtcgca atacgactca	6900
ctatagggcg aattgggtac cgggcccccc ctcgaggtcg acggtatcga taagcttgat	6960
atcgaattcc tgcagcccgg gggatccact agttctagag cggccgccac cgcggtggag	7020
ctccagcttt tgttcccttt agtgaggggt aatgctagaa atattttatc tgattaataa	7080
gatgatcttc ttgagatcgt tttggtctgc gcgtaatctc ttgctctgaa aacgaaaaaa	7140

ccgccttgca	gggcggtttt	tcgaagggttc	tctgagctac	caactctttg	aaccgaggta	7200
actggccttg	aggagcgcag	tcaccaaaac	ttgtcctttc	agtttagcct	taaccggcgc	7260
atgacttcaa	gactaactcc	tctaaatcaa	ttaccagtgg	ctgctgccag	tggtgctttt	7320
gcatgtcttt	cggggttga	ctcaagacga	tagttaccgg	ataaggcgca	gcggtcggac	7380
tgaacggggg	gttcgtgcat	acagtccagc	ttggagcgaa	ctgcctaccc	ggaactgagt	7440
gtcaggcgtg	gaatgagaca	aacgcggcca	taacagcgga	atgacaccgg	taaaccgaaa	7500
ggcaggaaca	ggagagcgca	cgagggagcc	gccaggggga	aacgcctggg	atctttatag	7560
tcctgtcggg	tttcgccacc	actgatttga	gcgtcagatt	tcgtgatgct	tgtcaggggg	7620
gcggagccta	tggaaaaacg	gctttgccgc	ggccctctca	cttcctgtt	aagtatcttc	7680
ctggcatctt	ccaggaaatc	tccgccccgt	tcgtaagcca	tttcgctcg	ccgcagtcga	7740
acgaccgagc	gtagcagagtc	agtgagcgag	gaagcggaat	atatcctgta	tcacatatct	7800
tgctgacgca	cgggtgcagc	cttttttctc	ctgccacatg	aagcacttca	ctgacaccct	7860
catcagtgcc	aacatagtaa	gccagtatac	actccgctag	cgctgatgtc	cggcgggtgt	7920
tttgccgtta	cgcaccaccc	cgtcagtagc	tgaacaggag	ggacagctga	tagaaacaga	7980
agccactgga	gcacctcaaa	aacaccatca	tacactaaat	cagtaagttg	gcagcatcac	8040
ccgacgcact	ttgcgccgaa	taaataacctg	tgacggaaga	tcacttcgca	gaataaataa	8100
atcctggtgt	ccctgttgat	accgggaagc	cctgggcca	cttttggcga	aaatgagacg	8160
ttgatcggca	cgtaagaggt	tccaactttc	accataatga	aataagatca	ctaccgggcg	8220
tattttttga	gttatcgaga	ttttcaggag	ctaagggaagc	taaaatggag	aaaaaatca	8280
ctggatatac	caccgttgat	atatcccaat	ggcatcgtaa	agaacatttt	gaggcatctt	8340
agtcagttgc	tcaatgtacc	tataaccaga	ccgttcagct	ggatattacg	gcctttttta	8400
agaccgtaaa	gaaaaataag	cacaagtttt	atccggcctt	tattcacatt	cttgcccgcc	8460
tgatgaatgc	tcatccggaa	ttccgtatgg	caatgaaaga	cggtgagctg	gtgatatggg	8520
atagtgttca	cccttgttac	accgttttcc	atgagcaaac	tgaaacgttt	tcatcgctct	8580
ggagtgaata	ccacgacgat	ttccggcagt	ttctacacat	atattcgcaa	gatgtggcgt	8640
gttacggtga	aaacctggcc	tatttcctta	aagggtttat	tgagaatatg	tttttcgtct	8700
cagccaatcc	ctgggtgagt	ttcaccagtt	ttgatttaaa	cgtggccaat	atggacaact	8760
tcttcgcccc	cgttttcacc	atgggcaa	attatacgca	aggcgacaag	gtgctgatgc	8820
cgctggcgat	tcaggttcat	catgccgtct	gtgatggctt	ccatgtcggc	agaatgctta	8880
atgaattaca	acagtactgc	gatgagtggc	agggcggggc	gtaatttttt	taaggcagtt	8940
attggtgccc	ttaaaccgct	ggtgctacgc	ctgaataagt	gataataagc	ggatgaatgg	9000

cagaaattcg aaagcaaatt cgacccggtc gtcgggttcag ggcaggggtcg ttaaataagcc 9060
 gcttatgtct attgctggtt taccggttta ttgactaccg gaagcagtgt gaccgtgtgc 9120
 ttctcaaattg cctgaggcca gtttgctcag gctctccccg tggaggtaat aattgacgat 9180
 atgatcattt attctgcctc ccagagcctg ataaaaacgg ttagcgcttc gttaatacag 9240
 atgtaggtgt tccacagggt agccagcagc atcctgcgat gcagatccgg aacataatgg 9300
 tgcagggcgc ttgtttcggc gtgggtatgg tggcaggccc cgtggccggg ggactgttgg 9360
 gcgctgccgg cacctgtcct acgagttgca tgataaagaa gacagtcata agtgccggcga 9420
 cgatagtcac gccccgcgcc caccggaagg agctaccgga cagcgggtgcg gactgttgta 9480
 actcagaata agaaatgagg ccgctcatgg cgttgactct cagtcatagt atcgtggtat 9540
 caccggttgg ttccactctc tgttgcgggc aacttcagca gcacgtaggg gacttccgcg 9600
 tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 9660
 acgttttgca gcagcagtcg cttcacgttc gctcgcgat cggtgattca ttctgctaac 9720
 cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 9780
 cccgtggcca ggacccaacg ctgcccga 9808

<210> 44
 <211> 26
 <212> PRT
 <213> *Listeria monocytogenes*

<400> 44

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp
 20 25

<210> 45
 <211> 59
 <212> PRT
 <213> *Listeria monocytogenes*

<400> 45

Met Thr Asp Lys Lys Ser Glu Asn Gln Thr Glu Lys Thr Glu Thr Lys
 1 5 10 15

Glu Asn Lys Gly Met Thr Arg Arg Glu Met Leu Lys Leu Ser Ala Val
 20 25 30

Ala Gly Thr Gly Ile Ala Val Gly Ala Thr Gly Leu Gly Thr Ile Leu

35

40

45

Asn Val Val Asp Gln Val Asp Lys Ala Leu Thr
 50 55

<210> 46
 <211> 53
 <212> PRT
 <213> Bacillus subtilillus

<400> 46

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
 1 5 10 15

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly
 20 25 30

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser
 35 40 45

Val Gly Ala Phe Gly
 50

<210> 47
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 47
 gtcaaaacat acgctcttat c 21

<210> 48
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 48
 acataatcag tccaaagtag atgc 24

<210> 49
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 49
ctctgggtacc tccttttgatt agtatattc 29

<210> 50
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
ctctggatcc atccgcgtgt ttcttttcg 29

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope insert

<400> 51
gattataaag atgatgatga taaa 24

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope

<400> 52

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epitope insert

<400> 53
gaacaaaaat taattagtga agaagattta 30

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope

<400> 54

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 55

<211> 9

<212> PRT

<213> Mus sp.

<400> 55

Ser Pro Ser Tyr Val Tyr His Gln Phe
1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope

<400> 56

Ser Pro Ser Tyr Ala Tyr His Gln Phe
1 5

<210> 57

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 57

ctctggtacc tcctttgatt agtatattc

29

<210> 58

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 58

caatggatcc ctcgagatca taatttactt catccc

36

<210> 59

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 59

atttctcgag tccatggggg gttctcatca tc 32

<210> 60

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 60

ggtgctcgag tgcggccgca agctt 25

<210> 61

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 61

cgattcccct agttatgttt accaccaatt tgctgca 37

<210> 62

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 62

gcaaattggt ggtaaacata actaggggaa t 31

<210> 63

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope insert

<400> 63

agtccaagtt atgcatatca tcaattt 27

<210> 64

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 64

cgatagtcca agttatgcat atcatcaatt tgc 33

<210> 65

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 65

gtcgcgcaaatt gatgatatgc ataacttgga ctat 34

<210> 66

<211> 8

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus Sequence

<220>

<221> misc_feature

<222> (1)..(1)

<223> n is a, c, g, or u

<400> 66

naggaggu 8

<210> 67

<211> 19

<212> DNA

<213> *Listeria monocytogenes*

<400> 67

aaggagagtg aaacccatg 19

<210> 68

<211> 240

<212> DNA

<213> *Listeria monocytogenes*

<400> 68

ggtacctcct ttgattagta tattcctatc ttaaagtgac ttttatgttg aggcattaac 60

at ttgttaac gacgataaag ggacagcagg actagaataa agctataaag caagcatata 120

atattgcgtt tcattctttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180

gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240

<210> 69
 <211> 240
 <212> DNA
 <213> *Listeria monocytogenes*

<400> 69
 ggtacctcct ttgattagta ttttcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattagggtt aaaaaatgta gaaggagagt gaaacccatg 240

<210> 70
 <211> 5
 <212> PRT
 <213> *Listeria monocytogenes*

<400> 70

Thr Glu Ala Lys Asp
 1 5

<210> 71
 <211> 5
 <212> PRT
 <213> *Listeria monocytogenes*

<400> 71

Asp Lys Ala Leu Thr
 1 5

<210> 72
 <211> 5
 <212> PRT
 <213> *Bacillus subtilus*

<400> 72

Val Gly Ala Phe Gly
 1 5